

GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 5, 2003, 02:50:22 ; Search time 1526 Seconds
(without alignments)
4669.734 Million cell updates/sec

Title: US-09-847-081B-2
Perfect score: 2270
Sequence: 1 MSXSVALLWVSTSEVSG.....IYAKSLVPPNRTSSPLAKT 440

Scoring table:
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlip
-O=/cgn2.1/USPTO.spool/US09847081/runat_01042003.120129.26749/app_query.fasta_1.583
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09847081 -CGN_1.1.2874.0runat_01042003.120129.26749 -NCPU=6 -ICPU=3
-NO_XLPV -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_inv:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1211	53.3	1655	11	AY11032	AY11032 Zea mays
2	1202	53.0	787	13	BM410846	BM410846 EST585173
3	1201.5	52.9	1201	11	AY108547	AY108547 Zea mays
4	1179	51.9	781	14	BQ511016	BQ511016 EST618431
5	1136	50.0	751	14	BQ046203	BQ046203 EST595321
6	1130	49.8	765	13	BM408984	BM408984 EST583311
7	1099	48.4	686	10	AW442101	AW442101 EST3111497
8	1083	47.7	682	13	BM409200	BM409200 EST583527
9	1072	47.2	672	10	AW442407	AW442407 EST3111803
10	1049	46.2	642	10	BE433198	BE433198 EST399727
11	1043	45.9	676	10	AW222027	AW222027 EST298838
12	1001	44.1	677	12	BG351357	BG351357 104A12 Ma
13	997	43.9	634	13	BM412533	BM412533 EST586660
14	980	43.2	600	10	BE460889	BE460889 EST412308
15	977.5	43.1	623	10	BE432511	BE432511 EST399040
16	956	42.1	685	10	AW221932	AW221932 EST298743
17	947	41.7	582	10	AW223316	AW223316 EST300127
18	940	41.4	581	10	BE432955	BE432955 EST399484
19	939	41.4	623	13	BM536249	BM536249 EST589271
20	934	41.1	582	10	AW223666	AW223666 EST300477
21	927	40.8	605	10	BE435064	BE435064 EST406142
22	927	40.8	744	13	BM412719	BM412719 EST587057
23	921	40.6	562	10	BE433966	BE433966 EST405044
24	918	40.4	634	13	BM137086	BM137086 WHE2629.C
25	917	40.4	565	10	BE432595	BE432595 EST399124
26	916	40.4	573	10	BE435308	BE435308 EST406386
27	913	40.2	585	10	AW222245	AW222245 EST299056
28	907	40.0	668	13	B1955682	B1955682 HVSME002
29	899	39.6	556	10	AW222152	AW222152 EST298963
30	897	39.5	609	10	BE322877	BE322877 NF048H11
31	891	39.3	581	10	AW222806	AW222806 EST299617
32	884	38.9	645	10	AW496851	AW496851 ga49602.Y
33	884	38.9	791	10	AW223528	AW223528 EST300339
34	881	38.8	542	10	BE431550	BE431550 EST336365
35	879	38.7	613	13	B1957464	B1957464 HVSME000
36	877	38.6	543	13	BM411875	BM411875 EST586202
37	873	38.5	634	10	AW441216	AW441216 EST310812
38	873	38.5	687	10	BE434578	BE434578 EST405656
39	870	38.3	542	10	BE432748	BE432748 EST399277
40	867	38.2	563	10	BE461396	BE461396 EST4112815
41	865	38.1	555	10	BE460463	BE460463 EST411882
42	860	37.9	566	12	BF112979	BF112979 EST440862
43	858	37.8	536	10	BE434911	BE434911 EST405989
44	856	37.7	563	10	BE437095	BE437095 EST408213
45	848	37.4	551	10	BE432084	BE432084 EST398613

ALIGNMENTS

RESULT 1
AY11032
LOCUS
DEFINITION Zea mays CL1906_1 mRNA sequence.
ACCESSION AY11032
VERSION AY11032.1 GI:21215622
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1655)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.


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|||||
Db 527 GTCTGGCGCTCGCTCCGACTCCAGGCTCGACCGAGCGTGATACATGCTGCTCTG 586
QY 300 AlaleuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319
Db 587 GCTCTCGGCATCGCTACACAGCTGACGAATATCTCAGAGACGTGGCGAAGATCGCAGG 646
QY 320 ArgGlyArgValTyLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
Db 647 AGGGGAGATATACCTTCGCTGGACGAGCTGCGGACGAGCTCTCAGCGAAGAGGAC 706
QY 340 IlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArg 359
Db 707 ATATTACAGGGAAGTGACCGCAAGTGGAGGAGGTTCATGAAGGCCAGATCCACGCT 766
QY 360 AlaArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArg 379
Db 767 GCCAGGCTCTCTTTGATGAGGCGGAGAGGCGTCAACCATCTCGACTCTGTAGCAGA 826
QY 380 TrpProValLeuThrAlaLeuLeuLeuTyArgLysIleLeuAspGluIleGluAlaAsn 399
Db 827 TGGCGGTGCTCGGCTCTGTGGCTGTACAGGCGATCCTTGATGCCATGTAGGCAAC 886
QY 400 AspTyAsnAsnPheThrArgArgAlaTyValSerLysProLysLysLeuLeuThrLeu 419
Db 887 GACTACAACAATTCACCAAGCGTGGTACGTCGGCAAGGCCAGAGAGCTGCTGCTGA 946
QY 420 ProIleAlaTyAlaLysSerLeuValProPro 430
Db 947 CCGCTTCATATGCAAGGCGTGGGTGCACCA 979

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RESULT 4

B0511016/c

LOCUS

DEFINITION

EST618431 Generation of a set of potato cDNA clones for microarray

analyses mixed potato tissues Solanum tuberosum cDNA clone STMH067

3' end, mRNA sequence.

B0511016

B0511016.2 GI:21926590

EST.

SOURCE

ORGANISM

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 781)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,

Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and

Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses

Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21369885.

Other ESTs: EST618430

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato@igr.org

This clone is available through the Research Genetics, contact the

Research Genetics for further information 1-800-711-6195 or

cdna@resgen.com

Seq primer: T7.

Location/Qualifiers

1..781

/organism="Solanum tuberosum"

/cultivar="Kennebec or Binjite"

/db_xref="taxon:4113"

/clone="STMH067"

/library="Generation of a set of potato cDNA clones for

microarray analyses mixed potato tissues"

/tissue_type="mixed tissues"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; supplier: Combination of untreated and Phytophthora

infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

BASE COUNT 202 a 191 c 144 g 244 t
ORIGIN

Alignment Scores:
Pred. No.: 4,78e-135 Length: 781
Score: 1179.00 Matches: 230
Percent Similarity: 96.36% Conservativeness: 8
Best Local Similarity: 93.12% Mismatches: 9
Query Match: 51.94% Indels: 1
DB: 14 Gaps: 0

US-09-847-081B-2 (1-440) x B0511016 (1-781)

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QY 194 AsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIle 213
Db 781 AATGCATCACACATACTCCACAGCTTTAGTAGTGGGAGGCCAGCTGGAAGATAT - 723
QY 214 PheSerGlyArgPropheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPhe 233
Db 722 TTCAACGGCGGCGCATTTGATATGCTTGATGTCAGCTTTATCCGATCTGTTTCCAAATT 663
QY 234 ProValAspIleGlnPropheArgAspMetIleGluGlyMetArgMetAspLeuTrpLys 253
Db 662 CCGTGTGATATTGAGCATTCAGAGATATGTTGAAAGGAATGCGTATGAGACTTGTGAAA 603
QY 254 SerArgTyrlLysThrPheAspGluLeuTyrlLeuTyrlCysTyrlValAlaGlyThrVal 273
Db 602 TCAGATACACAACACTTTGATGAACTATATCTATATGTTACTATGTCGTGTACAGTA 543
QY 274 GlyLeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSer 293
Db 542 GGATGTATGAGTGTTCATATTTATGGCATTGCACCTGAATCAAGGAACACACAGAGAGT 483
QY 294 ValTyrlAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAsp 313
Db 482 GTATATAACGACGCTTTGGCTTTAGGATCGCAAACTCAACTAATATATCTACTCAGAGAT 423
QY 314 ValGlyGluAspAlaArgArgGlyArgValTyrlLeuProGlnAspGluLeuAlaGlnAla 333
Db 422 GTAGGAGAAGATGCAAGAGAGGAGAGATATCTACTCAAGATGAATTAAGCACAGCA 363
QY 334 GlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTrpArgAsnPheMet 353
Db 362 GGGCTCTCCGATGAAGACATTTTGTGCTGGAAGAGTACTGATAAGTGGAGGATCTTTATG 303
QY 354 LysLysGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGlu 373
Db 302 AAGAAGCAAAATTCAGAGGGCAAGGAAATTTCTTGTATGAGGAGCAAGAAAGGTGTACAGAA 243
QY 374 LeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeuLeuTyrlArgLysIleLeu 393
Db 242 CTGAGCTCTGCTAGTAGTGGCGGTGTCGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTG 183
QY 394 AspGluIleGluAlaAsnAspTyrlAsnAsnPheThrArgArgAlaTyrlValSerLysPro 413
Db 182 GACGAGATTCAAGGCAAGCACTACAACAACCTTCAAGAGGAGGCTTATGTGAGCAAGCA 123
QY 414 LysLysLeuLeuThrLeuProIleAlaTyrlAlaLysSerLeuValProProAsnArgThr 433
Db 122 AAGAAGCTTCTGAGCTTGGCCCATTTGCTTATGCAAGATCTCTAGTGCCTCTAAGTCAACT 63
QY 434 SerSerProLeuAlaLysThr 440
Db 62 TCTTCCCACTAGCAAGACACA 42

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RESULT 5

B0046203

LOCUS

DEFINITION

EST595321 P. infestans-challenged potato leaf, incompatible

reaction Solanum tuberosum cDNA clone BPL114E21 5' end, mRNA

751 bp mRNA linear EST 29-MAR-2002

```

sequence.
BQ046203
VERSION BQ046203.1 GI:19820189
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
REFERENCE
AUTHORS Zhang,P., Hernandez,M., Tornqvist,C.-E., Wirtz,U., Loukianov,A.,
Rangel,P., Haberlach,G.T., Karanymcheva,S.A., Tsai,J., Chienmingo,A.,
Bougri,O., Buell,C.R., Ronning,C.M., Helgeson,J. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, incompatible interaction (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..751
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPL114E21"
/clone_lib="P. infestans-challenged potato leaf,
incompatible reaction"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: UC Berkeley, pGEC; sequencing: The
Institute for Genomic Research. Whole plants were
challenged with 450,000 sporangia/ml P. infestans isolate
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf
tissue was collected at 1, 2, 5, 12, and 24 hours
post-challenge and frozen in liquid nitrogen immediately
upon removal. Kennebec plants showed no signs of HR.
Katahdin plants (susceptible to P. infestans US-1) were
used as controls and showed infection. NOTE: We cannot
exclude the possibility that this sequence is actually
derived from Phytophthora rather than potato."
BASE COUNT 219 a 119 c 214 t
ORIGIN
Alignment Scores:
Pred. No.: 9.55e-130 Length: 751
Score: 1136.00 Matches: 225
Percent Similarity: 94.40% Conservative: 11
Best Local Similarity: 90.00% Mismatches: 12
Query Match: 50.04% Indels: 3
DB: 14 Gaps: 0
US-09-847-081b-2 (1-440) x BQ046203 (1-751)
Qy 67 AlaaspProArgTyrSerCysLeuGlyCysArgThrGluLysGlySerThrPheSer 86
Db 5 GCAGATTTCAGATATTCGTGTTTAGGAGATCAAGAACTGAGATGGAAGGATTTTCT 64
Qy 87 ValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSerSerGluLys 106
Db 65 GTACAGTCCAGTTGGTGGCTAGTCCAGCTGGAGAAATGGCTGTCTATCAGAAAAAG 124
Qy 107 ValTyraspValValLeuLysGlnAlaLeuValLysArgGlnLeuArgSerThrAsp 126
Db 125 GTGTATGAGGTGGTATTGAGCAGGACGCTTTAGTGAAGAGGCATCTGATATCTACTG 184
Qy 127 AspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAla 146
Db 185 GACATAGAAGTGAAGCCGGATATTGTTGTTCCCGGTAAATTTGGGCTTTGTTGTAAGCA 244
Qy 147 TyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLys 166
Db 245 TATGATCGTTGTGGGAGTAGTGTGCAGAGTATGCTAGACATTTTACTTAGGACCATG 304
Qy 167 LeuMetThrProGluArgArgAlaIleTrpAlaIleTyrValTyrPcysArgThr 186
Db 305 CTAATGACTCCAGACAGAGAAGAGCTATCTGGGCAATATATGTGTGGTGCAGGAACT 364
Qy 187 AspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrp 206
Db 365 GATGAGTTGTGTATGGCCCTTAATGATCACAATAAATCCACAAGCTTTAGATAGGTGG 424
Qy 207 GluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeu 226
Db 425 GAGCCAGGCTGGGAAGATATTTCAACGGCGGCCCATTTGATATGCTGTGATCGACCTT 484
Qy 227 SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly 246
Db 485 TCCGATACTGTTCCAAATTTCTGTTCATATTCAGCCATTTCAGAGATATGTTGAAGA 544
Qy 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCys 266
Db 545 ATGCGTATGGACTTGTGGAAATCCAGATACACAACATTTGATGAACATATATCTATTGT 604
Qy 267 TyrTyrValAlaGlyThrValGly-LeuMetSerValProValMetGlyIleAlaProGln 286
Db 605 TACTATGTCGCTGTACAGTAGGAATTGATGAGTGTTCATATTTGGCATTTGGACCTGA 564
Qy 286 userLysAlaThrThrGluSerValTyrAsnAlaAla-LeuAlaLeuGlyLeuAlaAsnG 306
Db 665 ATCCAAGGCAACAGACAGAGTGTATATAACGCAGCTTTTGGCTTTAGGGATCGCCAATC 724
Qy 306 InLeuThrAsnIleLeuArgAspVal 314
Db 725 AACTAACCAT-ATACTCAAGATGTA 749
RESULT 6
LOCUS BM408984 765 bp mRNA linear EST 22-JAN-2002
DEFINITION EST593311 tomato breaker fruit Lycopersicon esculentum cDNA clone
CUEG46P23 5' end, mRNA sequence.
ACCESSION BM408984
VERSION BM408984.1 GI:18260614
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 765)
AUTHORS Alcala,J., Vrebalov,J., White,R., Vision,T., Karanymcheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..765
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cUEG46P23"
/tissue_type="tomato breaker fruit"

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/dev_stage="breaker"
/lab_host="SOLR"
/notes=Vector: pBluescriptSKmCuadpt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp.
BASE COUNT      237 a      122 c      202 g      204 t
ORIGIN

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Alignment Scores:
Pred. No.:      5,45e-129      Length:      765
Score:          1130.00      Matches:      222
Percent Similarity: 90.94%      Conservative: 9
Best Local Similarity: 87.40%      Mismatches: 20
Query Match:      49.78%      Indels:      3
DB:              13      Gaps:      2

US-09-847-081B-2 (1-440) x BM408984 (1-765)

QY 128 LeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyr 147
Db 1 TTAGAAGTGAAGCGGATATACCTATTCCGGGGAATTTGGCTGTGTGAGTGAAGCATAT 60
QY 148 AspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeu 167
Db 61 GATAGGTGTGGTGAAGTATGTGCAGAGTATGCAAGACGTTTAACATTAGGAACATGCTA 120
QY 168 MetThrProGluArgArgAlaIleTyrAlaIleTyrValTyrCysArgGThrAsp 187
Db 121 ATGACTCCCGAGAGAGAGGCTATCTGGCAATATATATGTGGTGCAGAAACAGAT 180
QY 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTyrGlu 207
Db 181 GAACCTTGTATGCGCCAAACGATCATATATTACCCGCGACGCTAGATAGTGGAA 240
QY 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeuSer 227
Db 241 AATAGGCTAGAGATGTTTCAATGGCGGCCATTTGACATGCTCGATGCTGTGCTTC 300
QY 228 AspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMet 247
Db 301 GATACAGTTTCTTAACCTTCAGTATTCAGCCATTCAGACATATGATTTGAAGGATG 360
QY 248 ArgMetAspLeuThrLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyr 267
Db 361 CGTATGGACTTGAGAAATCGAGATACAAAACTTCGACGAACATATACCTTTATGTTAT 420
QY 268 TyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSer 287
Db 421 TATGTTCTGCTGAGGTGGTGTGATGAGTGTCCAAATATGTTGATCGCCCTGATCA 480
QY 288 LysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeu 307
Db 481 AAGCAACAACACAGAGCGTATATATGCTGCTTGGCTCTGGGATCGCAATCAATTA 540
QY 308 ThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeuProGln 327
Db 541 ACTAACATCTCAGAGATGTTGGGAAGATGCCAGAAGAGAGAGAGTCTACTTGCCTCAA 600
QY 328 AspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAs 347
Db 601 GATGAATTACACAGCGAGCTCTATCCGATGAAGATATATTTGCTGGAGAGGTGACCGA 660
QY 347 PLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaAlaGlySerPheAspGluSe 367
Db 661 TAAATGAGAGATCTTATGAGAAACAA---TACTAGGCAAGAAAGTCTTTCATGAGCA 717
QY 367 rGluLysGlyValThrGluLeuAspSerAlaSerArgTyr 380
Db 718 GAGAAAGCGT---GACAGATGAGCTCAGCTAGTATTC 754

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RESULT 7
AW442101      686 bp      mRNA      linear      EST 18-MAY-2001
LOCUS      EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
DEFINITION      clone cLEN21G20 5', mRNA sequence.
ACCESSION      AW442101
VERSION      AW442101.1 GI:6977352
KEYWORDS      EST.
SOURCE      tomato.
ORGANISM      Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE      1 (bases 1 to 686)
AUTHORS      Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F.,
Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Ronning, C. M.,
Fraser, C. M., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
1..686
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN21G20"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/notes=Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT      204 a      114 c      182 g      186 t
ORIGIN
Alignment Scores:
Pred. No.:      3.17e-125      Length:      686
Score:          1099.00      Matches:      209
Percent Similarity: 95.61%      Conservative: 9
Best Local Similarity: 91.67%      Mismatches: 10
Query Match:      48.41%      Indels:      0
DB:              10      Gaps:      0

US-09-847-081B-2 (1-440) x AW442101 (1-686)

QY 108 TyrAspValValLeuLysGlnAlaAlaLeuValLysArgGlnLeuArgSerThrAspAsp 127
Db 2 TATGATGTGTTTTTGAGCGAGGAGCGCTTGGTGAGAGGCACTGAGATCTACCAATGAG 61
QY 128 LeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyr 147
Db 62 TTAGAAGTGAAGCGGATATACCTATTCCGGGGAATTTGGCTGTGTGAGTGAAGCATAT 121
QY 148 AspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeu 167
Db 122 GATAGGTGTGGTGAAGTATGTGCAGAGTATGCAAGACGTTTAACATTAGGAACATGCTA 181
QY 168 MetThrProGluArgArgAlaIleTyrAlaIleTyrValTyrCysArgGThrAsp 187
Db 182 ATGACTCCCGAGAGAGAGGCTATCTGGCAATATATATGTGGTGCAGAAACAGAT 241

```

QY 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207
 Db 242 GAACTTTGTTGATGGCCCAACGCATCATATATACCCGCGCCTTAGATAGTGGGAA 301
 QY 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeuSer 227
 Db 302 ATAGGCTAGAGATGTTTCAATGGCGGCCATTGACATGCTCGATGGTCTTGTGCC 361
 QY 228 AspThrValSerArgProValAspIleGlnProPheArgAspMetIleGluGlyMet 247
 Db 362 GATACAGTTTCAACTTCCAGTTGATATACGCCATTGAGATATGATGGAAGATG 421
 QY 248 ArgMetAspLeuTrpLysSerArgTrpLysThrPheAspGluLeuTrpLysCysTrp 267
 Db 422 CGTATGGACTTGAGAAAATCGAGATACAAAACCTTCGACGAACATATACCTTTATTGTTAT 481
 QY 268 TyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSer 287
 Db 482 TATGTTGCTGGTACGGTTGGTGTGATGAGTGTTCNATTATGGGTATCCGCCCTGAATCA 541
 QY 288 LysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeu 307
 Db 542 AAGGCAACAACAGAGAGCGCTATATATGCTGCTTGGCTCTGGGATGCCAATCAATTA 601
 QY 308 ThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyrLeuProGln 327
 Db 602 ACTAATACTCAGAGATGTTGGAGAAGATGCCAGAAGAGGAGAGTCTACTTGCCTCAA 661
 QY 328 AspGluLeuAlaGlnAlaGlyLeu 335
 Db 662 GATGAATTAACCGACGAGTCTTA 685

RESULT 8

BM409200 682 bp mRNA linear EST 22-JAN-2002
 LOCUS EST583527 tomato breaker fruit Lycopersicon esculentum cDNA clone
 DEFINITION CLE847J1 5' end, mRNA sequence.

ACCESSION BM409200
 VERSION BM409200.1 GI:18260830
 KEYWORDS EST.
 SOURCE tomato.

ORGANISM

Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE

1 (bases 1 to 682)
 Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
 ,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
 ,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 Unpublished (2002)

COMMENT

Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.

FEATURES

source

Location/Qualifiers
 1..682
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEG47J1"
 /tissue.lib="tomato breaker fruit"
 /tissue.type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLN"
 /note="vector: pBluescriptSKmCUadapt; Site_1: EcoRI;
 Site_2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. Fruit
 were harvested at the breaker stage (first sign of
 lycopene accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp.

BASE COUNT 217 a 114 c 173 g 178 t

ORIGIN

Alignment Scores:

Pred. No.: 3 02e-123 Length: 682
 Score: 1083.00 Matches: 207
 Percent Similarity: 94.71% Conservative: 8
 Best Local Similarity: 91.19% Mismatches: 12
 Query Match: 47.71% Indels: 0
 DB: 13 Gaps: 0

US-09-847-081B-2 (1-440) x BM409200 (1-682)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgArg 174
 Db 1 GCAGAGTATGCAAGACGTTTAACTTAGGAACCTATGCTATGACTCCCGAGAGAAGG 60
 QY 175 AlaIleTrpAlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsn 194
 Db 61 GCTATCTGGGCAATATATGATGCTGCGAAGAACAGATGAACCTTGTGTGATGCCCAAC 120
 QY 195 AlaSerHisIleThrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePhe 214
 Db 121 GCATCATATATTACCCCGGCGCCCTTAGATAGTGGGAATAGGCTAGAGATGTTTC 180
 QY 215 SerGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPhePro 234
 Db 181 AATGGCGGCCATTTGACATGCTCGATGGTGTGCTTTGTCGATACAGTTTCTAACTTTCCA 240
 QY 235 ValAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSer 254
 Db 241 GTTGATATTTCAGCCATTCAGAGATATGATTGAAGGAATGCGTATGGACTTGCAGAAAATCG 300
 QY 255 ArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGly 274
 Db 301 ACATACAAAACCTTCGACGAACATATACCTTTATTTATTTGCTGCTGATCGGATGGG 360
 QY 275 LeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerVal 294
 Db 361 TTGATGAGTGTCCAATTATGGTATGCGCCCTGAATCAAAGGCAACAACAGAGAGCGTA 420
 QY 295 TyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspVal 314
 Db 421 TATAATGCTGCTTGGCTCTGGGGATCGCAAAATCAATTAACATACATCTCAGAGATGTT 480
 QY 315 GlyGluAspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGly 334
 Db 481 GGAGAAGATGCCAAGAGAGAGAGTCTCTTCCCTCAAGATGAATATATCACAGGAGGT 540
 QY 335 LeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLys 354
 Db 541 CTATCCGATGAGATATATTGCTGGAAGGTCACCGATAAATGGAGAACTTTATTCAG 600
 QY 355 LysGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGluLeu 374
 Db 601 AAACAAATACATAGGCAAGAAAGTCTTTTGTATGAGGAGAGAAAGCGGTGACAGAATTG 660
 QY 375 AspSerAlaSerArgTrpPro 381
 Db 661 AGCTCAGTAGTAGATTCCCT 681

RESULT 9

AW442407
 LOCUS AW442407
 DEFINITION EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 clone cLEN22L14 5', mRNA sequence.
 ACCESSION AW442407
 VERSION AW442407.1 GI:6977658

672 bp mRNA linear EST 18-MAY-2001

```

KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum.
REFERENCE 1 (bases 1 to 672)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
TITLE Generation of ESTs from tomato fruit tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Location/Qualifiers
1. 672
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN22L14"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 212 a 112 c 170 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 6.79e-122 Length: 672
Score: 1072.00 Matches: 205
Percent Similarity: 95.07% Conservative: 7
Best Local Similarity: 91.93% Mismatches: 11
Query Match: 47.22% Indels: 0
DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x AW442407 (1-672)

QY 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIle 179
Db 3 ACGTTAACTTAGGAACATGCTATATGATCCCGAGAGAAAGGCTATCTGGCAATA 62
QY 180 TyrValTyrCysArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199
Db 63 FATGTATGGTCGAGAGACAGATGACATGTTGTATGCCCAACAGCATCATATATACC 122
QY 200 ProGlnAlaLeuAspArgTTPgluThrArgLeuGluAspIlePheSerGlyArgProPhe 219
Db 123 CGGCAGCGCTTAGATAGTGGGAAATAGGCTAGAGATGTTTCAATGGCGGCATT 182
QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnPro 239
Db 183 GACATGCTCGATGGTGTTCGATACAGTTTCTCACTTTCCAGTTGATATTCAGCCA 242
QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPhe 259
Db 243 TTCACAGATATGATTGACAGATGCGTATGGACTTGAGAAATCCAGATACAAACATTC 302
QY 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279
Db 303 GACGAACATATACCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 362

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QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeu 299
Db 363 ATTATGGGTATCGCCCTGAATCAAGGCAACACAGAGAGCGTATATATCTGCTTTC 422
QY 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319
Db 423 GCTCTGGGATCGCAATCAATTAACATACTACAGATGTTTGGAGAAGATGCCAGA 482
QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
Db 483 AGAGGAAGAGTCTACTTGCCTCAAGATGAATAGCACAGAGCGTGTACGATGAAGAT 542
QY 340 IlePheAlaGlyArgValThrAspLysTyrArgAspPheMetLysLysGlnIleGlnArg 359
Db 543 ATATTGCTGGAGGGTGNCCGATAATGGAGAATCTTTATGAGAAACAATAACATAGG 602
QY 360 AlaArgLysPheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArg 379
Db 603 GCAGAAAGTCTTGTGATGAGGAGAAAGCGTGACAGAAATGAGCTCAGCTAGTAGA 662
QY 380 TrpProVal 382
Db 663 TTCCTGTGA 671

RESULT 10
LOCUS BE433198 642 bp mRNA linear EST 18-MAY-2001
DEFINITION ESN399727 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA
ACCESSION BE433198
VERSION BE433198.1 GI:9431041
KEYWORDS EST
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 642)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Niernan,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
1. 642
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG12N5"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKMuadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 194 a 103 c 167 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 4.47e-119 Length: 642
Score: 1049.00 Matches: 199

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Percent Similarity: 95.77% Conservative: 5
 Best Local Similarity: 93.43% Mismatches: 9
 Query Match: 46.21% Indels: 0
 DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x BE433198 (1-642)

QY 140 LeuGlyLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLys 159
 DB 2 TTGGGCTGTGAGTGAACCATATAGATAGTGTGGTGAAGATATGTCAGAGTATGCAAG 61
 QY 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPalAlle 179
 DB 62 ACCTTTAACTAGCACTATGCTATGATCTCCGAGAGAGAGGGCTATCTGGCAAT 121
 QY 180 TyrValTrpCysArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199
 DB 122 TATGTATGTCAGAGAACAGATGAACCTGTTGATGGCCCAACCATCATATATACC 181
 QY 200 ProGluAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPhe 219
 DB 182 CCGGCAGCCTTAGATAGTGGGAAATAGGCTAGAGATGCTTTCAATGGCGCCATTT 241
 QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnPro 239
 DB 242 GACATGCTCGATGGTCTTGTCCGATACAGTTCTTAACTTCCAGTTGATATTCAGCCA 301
 QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPhe 259
 DB 302 TTCAGAGATATGATTCAGGAATGCGTATGGACTTGAGAAATCGAGATACAAAACCTTC 361
 QY 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279
 DB 362 GACGAACATATACCTTATGTTATTTATGTTGCTGTGACGGTGGGTGATGAGTGTCCA 421
 QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 299
 DB 422 ATTTATGGGTATGCCCTCGAATCAAGGCAACACAGAGAGCGGTATATATGCTGTTG 481
 QY 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319
 DB 482 GCTCTGGGATGCCAATCAATTAATCACTACATCTACAGAGATGTTGGAGAAGTCCAGA 541
 QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
 DB 542 AGAGGAAGATCTACTTGGCTCAAGATGAATAGCACAGCAGGCTCTATCCGATGAAGAT 601
 QY 340 IlePheAlaGlyArgValThrAspLysTyrArgAsnPhe 352
 DB 602 ATATTTGCTGGAAGGTGACCGATAAATGGAGAATCTTT 640

RESULT 11
 AW222027
 LOCUS
 DEFINITION AW222027 676 bp mRNA linear EST 18-MAY-2001
 EST2988938 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 clone cLEN6L15, mRNA sequence.

ACCESSION
 VERSION AW222027
 KEYWORDS EST.

SOURCE
 ORGANISM

tomato.
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; eustersids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.

REFERENCE

AUTHORS
 Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
 Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 Generation of ESTs from tomato fruit tissue
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: CUGI
 Clemson University Genomics Institute

Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 Location/Qualifiers
 source
 1..676

/organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone_lib="cLEN6L15"
 /clone_lib="tomato fruit red ripe, TAMU"
 /tissue_type="pericarp"
 /dev_stage="red ripe (7-20 days post-breaker)"
 /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
 XhoI; supplier: Giovannoni; Fruit were tagged at the
 breaker stage (first sign of lycopene accumulation on the
 blossom end of the fruit) and harvested 7 days
 post-breaker (fully red-ripe), 10 days post breaker, and
 20 days post-breaker (over-ripe). 20 day fruit which
 showed external or internal signs of pathogenesis were
 discarded. Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

BASE COUNT 214 a 118 c 165 g 179 t
 ORIGIN

Alignment Scores:

Pred. No.: 2,69e-118 Length: 676
 Score: 1043.00 Matches: 201
 Percent Similarity: 94.64% Conservative: 11
 Best Local Similarity: 89.73% Mismatches: 12
 Query Match: 45.95% Indels: 0
 DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x AW222027 (1-676)

QY 189 LeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGluThr 208
 DB 2 CTGTGTGATGGCCCAACGCATCATATATACCCCGCAGCTTAGATAGTGGAAAT 61
 QY 209 ArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeuSerAsp 228
 DB 62 AGCTAGAGATGCTTTCAATGGCGGCCATTTGACATGCTCGATGCTGTTGTCGAT 121
 QY 229 ThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMetArg 248
 DB 122 ACAGTTTCTAACCTTCCAGTTGATATTCAGCCATTCAGAGATATGATGAGGAATCCGT 181
 QY 249 MetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyr 268
 DB 182 ATGGACTTGAGAAATCGAGATACAAAACCTTCGACGAACTATACCTTTATTGTTATTAT 241
 QY 269 ValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSerLys 288
 DB 242 GTTGTGTCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 301
 QY 289 AlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThr 308
 DB 302 GCAACACAGAGAGCGTATATATGCTGCTTGGCTCTGGGGATCGCAATCAATTAAC 361
 QY 309 AsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeuProGlnAsp 328
 DB 362 AACATCTCAGAGATGTTGAGAAGATGCCAAGAAGAGAGAGTCTACTTGCCTCAAGAT 421
 QY 329 GluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLys 348
 DB 422 GAATTAGCAGCAGCGTCTATCCGATGAAGATATATTTCTGCGAAGGTCGACCGATAA 481
 QY 349 TrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePheAspGluSerGlu 368
 DB 482 TGGAGATCTTTATGAAGAAACAATACATAGGCGCAAGAAAGTTCTTTGATGAGCGAGAG 541
 QY 369 LysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeu 388
 DB 369 LysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeu 388

sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 200 a 105 c 160 g 169 t

ORIGIN

Alignment Scores:

Pred. No.: 1,21e-112 Length: 634
Score: 997.00 Matches: 194
Percent Similarity: 94.31% Conservative: 5
Best Local Similarity: 91.94% Mismatches: 12
Query Match: 43.92% Indels: 1
DB: 13 Gaps: 0

US-09-847-081B-2 (1-440) x BM412533 (1-634)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174
DB 1 GCAGAGTATGCAAGACGCTTAACTAGGACTATGCTAACTGCTCCGAGAGAAAGG 60
QY 175 AlaLeuTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 194
DB 61 GCTATCTGGCCAAATATATGTTGTCAGAGAACAGATGAATGTTGATGGCCCAAC 120
QY 195 AlaSerHisIleThrProGluAlaLeuAspArgTTPGluThrArgLeuGluAspIlePhe 214
DB 121 GCATCATATATACCCGCGACCTTAGAGTGGGAAATAGGCTGAGAGATGTTTC 180
QY 215 SerGlyArgProPheAspMetLeuAspAlaLeuSerAspThrValSerArgPhePro 234
DB 181 AATGGCGGCCATTTGACATGCTCGATGCTGTTGTCGATACAGTTTCTAACTTCCA 240
QY 235 ValAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuThrPhe 254
DB 241 GTTGATATTCAGCCATTCAGAGATATGTTGAAGAAATCGCTATGAGAAATCG 300
QY 255 ArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGly 274
DB 301 AGATACAAAACCTTCGAGCACTATACCTTATTTGTTATGTTGCTGGTGGTGGG 360
QY 275 LeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerVal 294
DB 361 TTGATGAGTGTCCCAATATGTTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 295 TyrAsnAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspVal 314
DB 421 TATATGCTGCTTGGCTCTGGGATCGCAATCAATCAATCAATCAATCAATCAATCAAT 480
QY 315 GlyGluAspAlaArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGly 334
DB 481 GGAGAGATGCCAGAGAGAGAGATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 335 LeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrPheAsnPheMetLys 354
DB 541 CPTATCGATGAAGATATTTGCTGGAAGGTGACCATTAATGAGAATCTTTATGAAG 600
QY 355 LysGlnIleGlnArgAlaArgLysPheAsp 365
DB 601 AAACAATA-CATAGGGGCGAAGTCTTTGAT 632

RESULT 14
BE460889
LOCUS BE460889 600 bp mRNA linear EST 18-MAY-2001
DEFINITION ES412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE460889
VERSION BE460889.1 GI:9505191
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 600)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Niernm,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>

FEATURES
source

1..600
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLSG36H12"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI; Site 2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
BASE COUNT 178 a 99 c 157 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 1.42e-110 Length: 600
Score: 980.00 Matches: 185
Percent Similarity: 95.98% Conservative: 6
Best Local Similarity: 92.96% Mismatches: 8
Query Match: 43.17% Indels: 0
DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x BE460889 (1-600)

QY 137 ProGlyAsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGlu 156
DB 3 CGGGGAATTTGGGCTTGTGAGTGAATCATATGATAGGTGCTGAAGTGTGTGCAGAG 62
QY 157 TyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIle 176
DB 63 TATGCAAGACGCTTAACTTAGGAACATGCTAATCACTCCCGAGAGAGGGCTATC 122
QY 177 TrpAlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSer 196
DB 123 TGGGCAATATATGTTGTCAGAGAACAGATGAATGTTGATGCCCAACGATCA 182
QY 197 HisIleThrProGlnAlaLeuAspArgTTPGluThrArgLeuGluAspIlePheSerGly 216
DB 183 TATATACCCCGCAGCCCTTAGATAGTGGGAAATAGGCTAGAAATGTTTCAATGGG 242
QY 217 ArgProPheAspMetLeuAspAlaLeuSerAspThrValSerArgPheProValAsp 236
DB 243 CGGCCATTTGACATGCTCGATGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 302
QY 237 IleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuThrPheSerArgTyr 256
DB 303 ATTCAGCCATTCAGAGATATGTTGAAGGAATCGGTATGGACTTGAGAAATCGAGATC 362
QY 257 LysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMet 276
DB 363 AAAAATTCGACGAACTATACCTTTATTTATTTGCTGCTGCTGCTGCTGCTGCTGCTG 422
QY 277 SerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsn 296

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|||||...|||||
Db 423 AGTGTTCCAAATATGGTATCGCCCTGAATCAAGGCAACACAGAGCGCTATATAT 482
QY 297 AlalaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGlu 316
Db 483 GTGCTTTGGCTCTGGGGATCCCAATCAATTAACATACTACTCAGAGATGTTGGAGAA 542
QY 317 AspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeu 335
Db 543 GATGCCAGAGAGGAGAGAGTCTACTTGCTCAAGATGAATTAGCAGCAGCGTCTA 599

RESULT 15
BE432511
LOCUS
DEFINITION
  ESR399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
  clone cLE8H5, mRNA sequence.
ACCESSION
  BE432511
VERSION
  BE432511.1 GI:9430354
KEYWORDS
  EST.
SOURCE
  tomato.
ORGANISM
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
  Lycopersicon.
REFERENCE
  1 (bases 1 to 623)
  Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
  Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Renning,C.M.,
  Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
  ,S.D.
  Generation of ESTs from tomato fruit tissue, breaker stage
  Unpublished (2000)
  Contact: CUGI
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html
  5 prime sequence.
FEATURES
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    location/Qualifiers
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        /db_xref="taxon:4081"
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        /dev_stage="breaker"
        /lab_host="SOLR"
        /note="Vector: pBluescriptSKmCuadapt; Site_1: EcoRI;
        Site_2: XhoI; Fruit were harvested at the breaker stage
        (first sign of lycopen accumulation on the blossom end of
        the fruit). Fruit were cut in half and the seeds and
        locules were discarded prior to freezing the pericarp."
BASE COUNT
  191 a 101 c 164 g 167 t
ORIGIN

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Alignment Scores:

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Pred. No.:      3,08e-110      Length:      623
Score:          977.50         Matches:    190
Percent Similarity: 94.20%      Conservative: 5
Best Local Similarity: 91.79%   Mismatches: 10
Query Match:    43.06%         Indels:    2
DB:             10            Gaps:      1

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US-09-847-081B-2 (1-440) x BE432511 (1-623)

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QY 145 GluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGly 164
|||||...|||||
Db 3 GAAGCATATGATAGGTGTGGTCAAGTATGTGCAGAGATATGCAGAGACGTTTAACATGGA 62
QY 165 ThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyrValTrpCysArg 184
|||||...|||||
Db 63 ACTATGCTAATGACTCCCGAGAGAGAGGGCTATCTGGGCAATATATATGTGTGCAGA 122

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QY 195 ArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAsp 204
|||||...|||||
Db 123 AGACACAGATGAACCTTTGTTGATGGCCCAACGCGATCATATATTACCCCGCAGCCTTAGAT 182
QY 205 ArgTTPGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAla 224
|||||...|||||
Db 193 AGGTGGGAAATAGGCTAGAGATGTTTCAATGGGGGCCCATTTGCACATGCTCGATGGT 242
QY 225 AlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIle 244
|||||...|||||
Db 243 GCTTTGTCCGATACAGTTTCTTAACCTTCAGTTTGATATTACGCCATTTCAGAGATATGATT 302
QY 245 GluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeu 264
|||||...|||||
Db 303 GAAGGAATCGCGTATCGACTTTGAGAAATCGAGATACAAAACCTTCGACGAACTATACCTT 362
QY 265 Tyr---Cys-TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIle 283
|||||...|||||
Db 363 TATTGGTTAAATTTATGTTGCTGCTACGGTTGGGTTGATGAGTGTTCCAATTATGGGTAT 422
QY 283 ealaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLe 303
|||||...|||||
Db 423 CGCCCTGAATCAAAGGCAACAAACAGAGAGCGTATATATGCTGCTTGTGCTCTGGGAT 482
QY 303 uAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgVa 323
|||||...|||||
Db 483 CGCAATCAATTAACATACTACTCAGAGATGTTGGAGAAGATGCCAGAGAGAGAGAT 542
QY 323 lTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaG1 343
|||||...|||||
Db 543 CTACTTGGCTCAAGATGAATTAGCAGACGCGTCTATCCGATGAAGATATATTTGCTGG 602
QY 343 yArgValThrAspLysTrp 349
|||||...|||||
Db 603 GAGGCTGACCGATAAATGG 621

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Search completed: April 5, 2003, 04:26:44
 Job time : 1532 secs